

Dh	492	TGCTGATTAATCTCAAAATCTACATCAACGCGCGTGTGATCGACCGAAGAACGATCTC	555
Qy	552	caatctgggttaacatccacgggtttctataataacatcgttcaaaacttggaaggtgtgtctga	611
Dh	552	CAATCTGGGTTAACATCCACGGTCTTAATAATACATCATGTTCAACTGGACGGTGTGCTGA	611
Qy	612	cactcacgcgtacacatctggatcacaataacttcaactctgtctgcacaaagaacatgcgaaga	671
Dh	612	CACCTCACGCCCTCACTCTGATCGATCAAAATCTTCATCTGTTCGCAAAAGACATGAAACAAA	671
Qy	672	agaaatacaaaagacgctgtacgacaaacggtcccaatctctgtatccttgaaagaactctcggg	731
Dh	672	AGAAATCAAAAGACCTGTACGACAAACGGTCCCAATCTCTGTATCCTTGAAAGACTTCGGGG	731
Qy	732	tgactacacgtcagtaacgacaaacggtactacatcgtcgtaaactctgtatcagatccgaacaa	791
Dh	732	TGACTACACGTCAAGTACGACAAACCGTACTCATGCTGATCTGTACGATCCGAACAAAAT	791
Qy	792	cgcttgacgtcfaacaaatgataaggtatccgcgggttcaacatgtaacggaaggctccgggtgtc	851
Dh	792	CGCTTGACGTCFAACAATGTAGATATCCCGGTTACATATACCTGAAAGGCTCCGCTGGTGT	851
Qy	852	tgctatgactaccaaactcactcactgaaactctccctcgtatccggtgtgatacccaatlcata	911
Dh	852	TGTTATGACTTACCAACATCTACCTGAACCTTCCGTAACGCTGTGTACCAAAATTCATCAT	911
Qy	912	caagaaatacgcgctctgtgttaacaagaagacaaatgcttgcgaagaagatgctgtatacat	971
Dh	912	CAGAAATACGCGCTTGGTGTGAACAAAGACAAATATCTGTCACAAACATATATCGTGTATCAT	971
Qy	972	caatgtctagtgtaaaagaacaaagaatacgcgtctggtcaccatgctcttcacaggctggtgt	1031
Dh	972	CAATGTCTAGTGAAGAAACAAAGAAATACGCTGTGCTACCAATCTCTCAGCCTGTGT	1031
Qy	1032	agaaaagaactctgtctctgtctcgtgaatcccggaacgtttgatactgtctcgaagtagtgt	1091
Dh	1032	AGAAAAGAACTCTGTCTGTCTGTGAAATCCCGAACGTTGTGTATCTGTCTCAGTACTTGT	1091
Qy	1092	aatgaaatccaaagaacgacgaggtatcactacaacaatgacaatgaaactctgcagagaca	1151
Dh	1092	AATGAAATCCAAAGAACGCCAGGTTATCACTAAACAAATGCAAAATGAAATCTGCAGACAAA	1151
Qy	1152	caatgttaacgatacgtgttcaatcgtgttccacagatctcaacaatactgcctaacttgt	1211
Dh	1152	CATGTGTAACTATCCGTTTCAATCCGTTTCCACAGTTCAACAATATCCCTAAACTGT	1211
Qy	1212	tgcttccaaactggtatacaatcgtcagaatcgaaagctctccctccgcaccttggtgtgctctg	1271
Dh	1212	TGCTTCCAACTGCTACATCTCTAGATCGAAAGTTCTCTCTGCACTGTGGCTGTGCTTGT	1271
Qy	1272	ggagttcaccccggtctgtatgcaggtctgggggtgaacgctgcgctgttaa	1317
Dh	1272	GGAGTTCACTCCCGTGTATGTATGACGGTGTGGGTGAAGCTGCCGTGTAA	1317
RESULT 4			
US-08-480-604A-25			
Sequence 25 Application US/08480604A			
Patent No. 5736139			
GENERAL INFORMATION:			
APPLICANT: KINK, JOHN A.			
APPLICANT: THALLEY, BRUCE S.			
APPLICANT: PADHIE, NISHA V.			
APPLICANT: FIRCH, JOSEPH R.			
APPLICANT: STAFFORD, DOUGLAS C.			
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND			
PREVENTION OF C. DIFFICILE DISEASE			
NUMBER OF SEQUENCES: 32			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: MEDLIN & CARROLL, LLP			
STREET: 220 MONTGOMERY STREET, SUITE 2200			
CITY: SAN FRANCISCO			
STATE: CALIFORNIA			





## RESULT 6

US-08-915-136-25

Sequence 25, Application US/08915136

Patent No. 6290960

## GENERAL INFORMATION:

APPLICANT: KINK, JOHN A.

APPLICANT: THALEY, BRUCE S.

APPLICANT: PADHYE, NISHA V.

APPLICANT: FIRCA, JOSEPH R.

APPLICANT: STAFFORD, DOUGLAS C.

TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND

PREVENTION OF C. DIFFICILE DISEASE

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: MEDLEN &amp; CARROLL, LLP

STREET: 220 MONTGOMERY STREET, SUITE 2200

CITY: SAN FRANCISCO

STATE: CALIFORNIA

COUNTRY: UNITED STATES OF AMERICA

ZIP: 94104

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/915,136

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/480,604

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/405,496

FILING DATE: 16-MAR-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/329,154

FILING DATE: 25-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/161,907

FILING DATE: 02-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/985,321

FILING DATE: 04-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/429,791

FILING DATE: 31-OCT-1989

ATTORNEY/AGENT INFORMATION:

NAME: INGOLTA, DIANE E.

REGISTRATION NUMBER: 40,027

REFERENCE/DOCKET NUMBER: OPHD-01763

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 705-8410

TELEFAX: (415) 397-8338

INFORMATION FOR SEQ ID NO: 25:

SEQUENCE CHARACTERISTICS:

LENGTH: 1402 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..1386

US-08-915-136-25

Query Match 98.6%; Score 1304.4; DB 4; Length 1402;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1305; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 gatgtctactccttcgaatatacgaacatcatcatcaccctcgaaccctgag 71

|||||

Db 84 gctgtctactccttcgaatatacgaacatcatcatcaccctcgaaccctgag 143

Qy 72 ctacgaatcccaatccacccgtatcgacccgtctcgtctcgtctcgtctcgtctc 131

Db 144 ctacgaatcccaatccacccgtatcgacccgtctcgtctcgtctcgtctcgtctc 203

Qy 132 taagtttaacttcgatccgatccgaacaaatccgatccgatccgatccgatcc 191

Db 204 taaagtttaacttcgatccgatccgaacaaatccgatccgatccgatccgatcc 263

Qy 192 caaaatcgaagttaacttcgatccgaacaaatccgatccgatccgatccgatcc 251

Db 264 caaaatcgaagttaacttcgatccgaacaaatccgatccgatccgatccgatcc 323

Qy 252 caactccttcgtgatccgatccgaacaaatccgatccgatccgatccgatcc 311

Db 324 caactccttcgtgatccgatccgaacaaatccgatccgatccgatccgatcc 383

Qy 312 caactccttcgtgatccgatccgaacaaatccgatccgatccgatccgatcc 371

Db 384 caactccttcgtgatccgatccgaacaaatccgatccgatccgatccgatcc 443

Qy 372 aatcattcgtgatccgatccgaacaaatccgatccgatccgatccgatcc 431

Db 444 aatcattcgtgatccgatccgaacaaatccgatccgatccgatccgatcc 503

Qy 432 tcaagttaacttcgatccgaacaaatccgatccgatccgatccgatcc 491

Db 504 tcaagttaacttcgatccgaacaaatccgatccgatccgatccgatcc 563

Qy 492 tcaagttaacttcgatccgaacaaatccgatccgatccgatccgatcc 551

Db 564 tcaagttaacttcgatccgaacaaatccgatccgatccgatccgatcc 623

Qy 552 caactcgttgatccgaacaaatccgatccgatccgatccgatccgatcc 611

Db 624 caactcgttgatccgaacaaatccgatccgatccgatccgatccgatcc 683

Qy 612 caactcgttgatccgaacaaatccgatccgatccgatccgatccgatcc 671

Db 684 caactcgttgatccgaacaaatccgatccgatccgatccgatccgatcc 743

Qy 672 agaaatcgaacaaatccgatccgaacaaatccgatccgatccgatccgatcc 731

Db 744 agaaatcgaacaaatccgatccgaacaaatccgatccgatccgatccgatcc 803

Qy 732 tgaactcgttgatccgaacaaatccgatccgatccgatccgatccgatcc 791

Db 804 tgaactcgttgatccgaacaaatccgatccgatccgatccgatccgatcc 863

Qy 792 cgttgatccgaacaaatccgatccgaacaaatccgatccgatccgatccgatcc 851

Db 864 cgttgatccgaacaaatccgatccgaacaaatccgatccgatccgatccgatcc 923

Qy 852 tgaactcgttgatccgaacaaatccgatccgatccgatccgatccgatcc 911

Db 924 tgaactcgttgatccgaacaaatccgatccgatccgatccgatccgatcc 983

Qy 912 caagaatcgaacaaatccgatccgaacaaatccgatccgatccgatccgatcc 971

Db 984 caagaatcgaacaaatccgatccgaacaaatccgatccgatccgatccgatcc 1043

Qy 972 caagtctgtaagtaagaacaaatccgatccgatccgatccgatccgatcc 1031

Db 1044 caagtctgtaagtaagaacaaatccgatccgatccgatccgatccgatcc 1103

Qy 1032 agaaatcgaacaaatccgatccgaacaaatccgatccgatccgatccgatcc 1091

Db 1104 agaaatcgaacaaatccgatccgaacaaatccgatccgatccgatccgatcc 1163

Qy 1092 aatgaatcgaacaaatccgatccgaacaaatccgatccgatccgatccgatcc 1151

Db 1164 aatgaatcgaacaaatccgatccgaacaaatccgatccgatccgatccgatcc 1223

```

COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,604A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/422,711
FILING DATE: 14-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/405,496
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,154
FILING DATE: 25-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: INGOLIA, DIANE E.
REGISTRATION NUMBER: 40,0027
REFERENCE/DOCKET NUMBER: OPND-01763
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 1402 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1386
US-08-480-604A-25
Query Match 98.4%; Score 1311; DB 1; Length 1402;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1311; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 316 gaatacaccatcaactgcagtaagaacaattcgtgtgaaaglatcctgaactac 375
DB 379 GAATACACCATCATCACTGATGCAAAACAAATCTGTTGGAAGATATCTGAACTAC 438
OY 376 gttgaatcatctggaactctgcaagacactcaggaaatacaagagctgttgaattcaa 435
DB 439 GGTGAATCATCTGCACTCTGCAAGACACTCAGAAATCAAAACGCTGTGATTCAAA 498
OY 436 tactcagaatcaacaatctcgaatacaatcgcgtgagatctcgttaaccatcac 495
DB 499 TACTCTCAATGATCAATCAATCTCTGATCAATCAATGATGATCTCTGATCAATCAC 558
OY 496 aacaatcgtctgaataacttcaaaatactcaatcaagagcgtctgtaaccagaacccg 555
DB 559 AACATCGCTGTAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 618
OY 556 atctccaatctggtgaatcaatcgaactcgaatacaatcgaatcgaatcgaatcga 615
DB 619 ATCTCCAATCTGTTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 678
OY 616 atctgaactcgaactcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 675
DB 679 CGTGAACCTCACCCTGATCTGATCAATCAATCAATCAATCAATCAATCAATCAATCA 738
OY 676 gaaagaagaatcaagaactcgtgaagaacagttcgaatcgtgaatcgtgaatcgtga 735
DB 739 GAAAGAAGAATCAAGAACTGATCAATCAATCAATCAATCAATCAATCAATCAATCA 798
OY 736 tgggtgactcactcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 795
DB 799 TGGGTGACTCTGATCTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 858
OY 796 aatacagctgacgtcaacaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 855
DB 859 AATACAGCTGACGTCAACAATCAATCAATCAATCAATCAATCAATCAATCAATCA 918
OY 856 gttcgtctatgactcaacaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 915
DB 919 GTTCTGTTATGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 978
OY 916 atcattagaagaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 975
DB 979 ATCATGAAGAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1038
OY 976 tacatcaatctgtagtcaagaacaagaatacgtctgtaaccatcgtctcgaatcga 1035
DB 1039 TACATCAATCTGTTGATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 1098
OY 1036 ggtgtagaagaatcgtctgctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 1095
DB 1099 GGTGTGAAGAATCTTGTCTGCTCTGCAAAATCCCGGACGTTGATCTGTTCAAGTA 1158
OY 1096 gttgtaataaatacgaagaacgaggtatcactcaacaatacgaagaatacgtcga 1155
DB 1159 GTTGTATATGAATCAAGAACGACGAGGTATCACTAAACAAATGAATGATGCGAG 1218
OY 1156 gacaacaatgtaacgaatcgtctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 1215
DB 1219 GACAACAATGTAACGAATCGGTTTCAATCGTTTCAACAGTTCAACATATTCGTTAA 1278
OY 1216 ctggtctcctcaactcgttacaatcgttacaatcgttacaatcgttacaatcgttaca 1275
DB 1279 CTGTTCTCTCAACTGATGATCAATCGTCAATCGTCAATCGTCAATCGTCAATCGTCA 1338
OY 1276 tcttggaatcattaccggtctgtagaagcgttgggtgtagaagcgtcgtcgtcgtcgtc 1326
DB 1339 TCTTGGAATTCATCCGCTGATGATGACGTTGGGTGAACGTCCGCTGTAA 1389

```

RESULT 5  
 US-08-405-496A-25  
 ; Sequence 25, Application US/08405496A  
 ; Patent No. 591965

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

## OM nucleic - nucleic search, using sw model

Run on: September 16, 2002, 21:32:06 : Search time 139.08 Seconds

(without alignments)  
2336.391 Million cell updates/sec

Title: US-09-611-419a-3

Perfect score: 1323

Sequence: 1 gaattcgaacagatgctctac.....aacgtccgcgtgaagattc 1323

Scoring table: IDENTITY-NUC

Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

- Issued Patents NA: \*
- 1: /cgn2\_6/prodata/2/lna/5A.COMB.seq:\*
  - 2: /cgn2\_6/prodata/2/lna/5B.COMB.seq:\*
  - 3: /cgn2\_6/prodata/2/lna/5A.COMB.seq:\*
  - 4: /cgn2\_6/prodata/2/lna/5B.COMB.seq:\*
  - 5: /cgn2\_6/prodata/2/lna/5A.COMB.seq:\*
  - 6: /cgn2\_6/prodata/2/lna/5B.COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1304.4	98.6	1330	1	US-08-480-604A-22
2	1304.4	98.6	1330	2	US-08-405-496A-22
3	1304.4	98.6	1330	4	US-08-915-136-22
4	1304.4	98.6	1402	1	US-08-480-604A-25
5	1304.4	98.6	1402	2	US-08-405-496A-25
6	1304.4	98.6	1402	4	US-08-915-136-25
7	726.4	54.9	3891	1	US-08-480-604A-27
8	726.4	54.9	3891	2	US-08-405-496A-27
9	726.4	54.9	3891	4	US-08-915-136-27
10	166.4	12.6	1359	1	US-07-618-312A-3
11	166.4	12.6	1359	1	US-08-280-228-3
12	74.2	3.6	1359	1	US-07-618-312A-1
13	74.2	3.6	1359	1	US-08-110-786A-7
14	74.2	3.6	1359	1	US-08-280-228-1
15	74.2	3.6	1359	1	US-08-668-381A-6
16	60	4.5	5511	3	US-08-928-361B-2
17	60	4.5	5511	3	US-08-928-361B-1
18	57	4.3	5163	3	US-08-700-651-1
19	57	4.3	5163	3	US-08-700-651-2
20	57	4.3	5163	3	US-08-700-651-3
21	57	4.3	5163	3	US-08-700-651-4
22	40	3.0	1690	2	US-08-798-744-24
23	40	3.0	1690	2	US-08-798-744-24
24	37.8	2.9	2277	1	US-08-676-967-2
25	37.8	2.9	2277	1	US-08-676-967-2
26	37.8	2.9	2277	2	US-09-098-487-2
27	37.2	2.8	18596	4	US-09-318-448-11

28	36.8	2.8	1430	1	US-08-276-452A-25	Sequence 25, Appl
29	36.8	2.8	1430	2	US-08-798-744-25	Sequence 25, Appl
30	34.6	2.6	2094	3	US-08-714-918-87	Sequence 87, Appl
31	34.6	2.6	2094	4	US-09-265-315-87	Sequence 87, Appl
32	34.6	2.6	2094	4	US-09-265-315-87	Sequence 87, Appl
33	34.6	2.6	2094	4	US-09-265-315-87	Sequence 87, Appl
34	34.6	2.6	2094	4	US-09-265-315-87	Sequence 87, Appl
35	34.4	2.6	951	1	US-07-855-412B-2	Sequence 2, Appl
36	34.4	2.6	951	2	US-08-881-094-2	Sequence 2, Appl
37	34.2	2.6	198	5	PCT-US95-10668-1	Sequence 2, Appl
38	34.2	2.6	198	5	PCT-US95-10668-2	Sequence 2, Appl
39	34.2	2.6	198	5	PCT-US95-10668-3	Sequence 2, Appl
40	34.2	2.6	198	5	PCT-US95-10668-4	Sequence 2, Appl
41	34.2	2.6	3292	1	US-07-814-964-12	Sequence 12, Appl
42	34.2	2.6	3292	1	US-08-258-442-12	Sequence 12, Appl
43	34.2	2.6	3292	1	US-08-328-809-7	Sequence 12, Appl
44	34.2	2.6	3292	5	PCT-US97-11107-12	Sequence 12, Appl
45	34	2.6	1666	4	US-09-134-607A-8	Sequence 8, Appl

## ALIGNMENTS

RESULT 1  
US-08-480-604A-22  
Sequence 22, Appl  
Patent No. 5736139  
Application US/08480604A  
GENERAL INFORMATION:  
APPLICANT: KINK, JOHN A.  
APPLICANT: THALLEY, BRUCE S.  
APPLICANT: PADHYE, NISHA V.  
APPLICANT: FTRCA, JOSEPH R.  
APPLICANT: STAFFORD, DOUGLAS C.  
TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND PREVENTION OF C. DIFFICILE DISEASE  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: MEDLEN & CARROLL, LLP  
STREET: 220 MONTGOMERY STREET, SUITE 2200  
CITY: SAN FRANCISCO  
STATE: CALIFORNIA  
COUNTRY: UNITED STATES OF AMERICA  
ZIP: 94104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/480,604A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/422,711  
FILING DATE: 14-APR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/405,496  
FILING DATE: 16-MAR-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/329,154  
FILING DATE: 25-OCT-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/161,907  
FILING DATE: 02-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/985,321  
FILING DATE: 04-DEC-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/429,791  
FILING DATE: 31-OCT-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: INGOLIA, DIANE E.  
REGISTRATION NUMBER: 40,027

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic acid search, using sw model

Run on: September 16, 2002, 21:29:41 ; Search time 7254.67 Seconds

(without alignments)  
3816.274 Million cell updates/sec

Title: US-09-611-419A-3

Perfect score: 1323  
Sequence: 1 gaattcgaaagatgctctac.....aacgtccgtctgaagatc 1323

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :  
1: gb\_ba:\*  
2: gb\_hlg:\*  
3: gb\_hn:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sgs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sgs:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hlg\_hum:\*  
31: em\_hlg\_inv:\*  
32: em\_hlg\_other:\*  
33: em\_higo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result Query  
No. Score Match Length DB ID Description

1	1304.4	98.6	1330	6	AR000029	AR000029 Sequence
2	1304.4	98.6	1330	6	AR169140	AR169140 Sequence
3	1304.4	98.6	1330	6	AX036243	AX036243 Sequence
4	1304.4	98.6	1338	12	XU22962	XU22962 Synthetic b
5	1304.4	98.6	1402	6	AR000030	AR000030 Sequence
6	1304.4	98.6	1402	6	AR169141	AR169141 Sequence
7	1304.4	98.6	1402	6	AX036246	AX036246 Sequence
8	727.6	55.0	4292	1	CBOTAG	X52066 Clostridium
9	727.6	54.9	4835	1	CLOEHR	M30196 C. botulinum
10	726.4	54.9	3891	6	AR000031	AR000031 Sequence
11	726.4	54.9	3891	6	AR169142	AR169142 Sequence
12	726.4	54.9	3891	6	AX036248	AX036248 Sequence
13	662	50.0	4067	1	CBMTOX	X73423 C. botulinum
14	423.2	32.0	1299	12	AF251281	AF251281 Synthetic
15	421.6	31.9	1313	6	A58946	A58946 Sequence 6
16	228	17.2	4073	1	CBONTF	X68262 C. baratti ge
17	227	17.2	1293	6	A58945	A58945 Sequence 5
18	227	17.2	4199	1	CLOBONT	L35496 Clostridium
19	227	17.2	4209	1	CBONTFG	X81714 C. botulinum
20	195.8	14.8	3835	1	AB037704	AB037704 Clostridi
21	195.8	14.8	3835	1	AB037705	AB037705 Clostridi
22	195.8	14.8	3835	1	AB037706	AB037706 Clostridi
23	195.8	14.8	3835	1	AB037707	AB037707 Clostridi
24	195.8	14.8	3835	1	AB037708	AB037708 Clostridi
25	195.8	14.8	3835	1	AB037709	AB037709 Clostridi
26	195.8	14.8	3835	1	AB037710	AB037710 Clostridi
27	195.8	14.8	3835	1	AB037711	AB037711 Clostridi
28	195.8	14.8	3835	1	AB037712	AB037712 Clostridi
29	195.8	14.8	3835	1	AB037713	AB037713 Clostridi
30	195.8	14.8	3835	1	AB037714	AB037714 Clostridi
31	195.8	14.8	4030	1	CBNTTE	X63683 C. botulinum
32	194.2	14.7	4017	6	CBNTTOXE	X62085 C. botulinum
33	194.2	14.7	4017	6	AX088262	AX088262 Sequence
34	191	14.4	3838	1	AB039264	AB039264 Clostridi
35	191	14.4	3949	1	CBNTTE	X62088 C. butyricum
36	180.8	13.7	4234	1	CLOEHR	M92906 Clostridium
37	180.8	13.7	9325	1	CBY13631	Y13631 Clostridium
38	166.4	12.6	1359	6	I28431	I28431 Sequence 3
39	166.4	12.6	3712	6	A49987	A49987 Sequence 4
40	166.4	12.6	3754	6	A37074	A37074 Sequence 17
41	166.4	12.6	3754	6	A42478	A42478 Sequence 6
42	166.4	12.6	3769	6	A37075	A37075 Sequence 18
43	166.4	12.6	3769	6	A49988	A49988 Sequence 5
44	166.4	12.6	4366	6	A42484	A42484 Sequence 12
45	166.4	12.6	4378	6	A42481	A42481 Sequence 9

## ALIGNMENTS

RESULT 1  
AR000029 AR000029 1330 bp DNA linear PAT 04-DEC-1998  
LOCUS Sequence 22 from patent US 5736139.  
DEFINITION AR000029  
ACCESSION AR000029.1 GI:3962560  
VERSION  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1330)  
AUTHORS Kink, J.A., Thalley, B.S., Stafford, D.C., Pirca, J.R. and Padhye, N.V.  
TITLE Treatment of Clostridium difficile induced disease  
JOURNAL Patent: US 5736139-A 22 07-APR-1998;  
FEATURES  
source Location/Qualifiers  
1..1330  
BASE COUNT 400 a 339 c 246 g 345 t  
ORIGIN

Query Match 98.6%; Score 1304.4; DB 6; Length 1330;  
Best Local Similarity 99.9%; Pred. No. 0;

SEQID 3



Matches 1305; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy	12	gaagctacacctccactgaataataataagaataataataaacctccactctggaactgtg	71
Db	12	gcgtctacgttccactgaactgaatracatcaagaacatcatatccctccatcctgaacctgg	71
Oy	72	ctagaataccaatacaactgtatcgacctgtcccgctgaagctccaaaatacaactgtgtc	131
Db	72	ctacgaatccaatcacctgtatcgacctgtcccgctgaagctccaaaatacaactgtgtc	131
Oy	132	taaaagcttaactctgcataccgatacgacaagaatacagaatccagctgtccaaatctgc	191
Db	132	taaaagtttaactctgcataccgataccagaagaatcagatccagctgttcctgaatctgtc	191
Oy	192	caaaatacgaagaattctctggaagaattctctgtataaacaactctgtgaagaactcttc	251
Db	192	caaaatacgaagaattctctggaagaattctctgtataaacaactctgtgaagaactcttc	251
Oy	252	caactccctctgtagatcgatataccgaataacttcaactccatctctctgacaatgata	311
Db	252	caactccctctgtagatcgatataccgaataacttcaactccatctctctgacaatgata	311
Oy	312	caaccatcatcaactcgatctggaataaacaactctgtgtggaagaatactctgaaactgtga	371
Db	312	caaccatcatcaactcgatctggaataaacaactctgtgtggaagaatactctgaaactgtga	371
Oy	372	aaatcaatctggaactctgcaagaacatccgaagaatacaaaagctgtgtatccaactctc	431
Db	372	aaatcaatctggaactctgcaagaacatccgaagaatacaaaagctgtgtatccaactctc	431
Oy	432	tcagaatgatacaatctctctgaatacaactcgaactgtgtatctctgataccaacaaca	491
Db	432	tcagaatgatacaatctctctgaatacaactcgaactgtgtatctctgataccaacaaca	491
Oy	492	tcgtctggaataaactccaaataatacaaaagcgcgtctgtatcgacaagaacacgatactc	551
Db	492	tcgtctggaataaactccaaataatacaaaagcgcgtctgtatcgacaagaacacgatactc	551
Oy	552	caatctggtgaatccatccaaactctcaataactcaatgttcaaaactgtgaagcgtgtcgtga	611
Db	552	caatctggtgaatccatccaaactctcaataactcaatgttcaaaactgtgaagcgtgtcgtga	611
Oy	612	caactcaacgctatactctgtgatacaaaacttcaactctgtctcgacaagaatactgaagaana	671
Db	612	caactcaacgctatactctgtgatacaaaacttcaactctgtctcgacaagaatactgaagaana	671
Oy	672	agaaatacaaaagcgcgtatacagaacaacagatccaaatctgtatactctgaaagaactctcg	731
Db	672	agaaatacaaaagcgcgtatacagaacaacagatccaaatctgtatactctgaaagaactctcg	731
Oy	732	tgactactctgcatgatacgaacaacgctatacaatctgtctgataactctgtagaatcgacaata	791
Db	732	tgactactctgcatgatacgaacaacgctatacaatctgtctgataactctgtagaatcgacaata	791
Oy	792	cgttcgactgaacaatactgaagatactcgcgcggtatactgaactctgaaagaagctcgcgtgttc	851
Db	792	cgttcgactgaacaatactgaagatactcgcgcggtatactgaactctgaaagaagctcgcgtgttc	851
Oy	852	tgtttatgactgaacaatactgaagatactcgcgcggtatactgaactctgaaagaagctcgcgtgttc	911
Db	852	tgtttatgactgaacaatactgaagatactcgcgcggtatactgaactctgaaagaagctcgcgtgttc	911
Oy	912	caagaatactcgctctgtgatacaagaacatactgtctgcgaacaatgatactgtatatacat	971
Db	912	caagaatactcgctctgtgatacaagaacatactgtctgcgaacaatgatactgtatatacat	971
Oy	972	caactctctgaatgaagaacaagaatactgtctgtctatacaaatgtctcttaagcctgtgt	1031
Db	972	caactctctgaatgaagaacaagaatactgtctgtctatacaaatgtctcttaagcctgtgt	1031
Oy	1032	agaaagaatctgtctgtctctgtgaaatacccggaagctgtgtaaactgtctcaagtagtgt	1091
Db	1032	agaaagaatctgtctgtctctgtgaaatacccggaagctgtgtaaactgtctcaagtagtgt	1091

Oy	1092	aagaaatccaaagaagacaaaggtatcaactcaaaatgcaaaatgaatctcagagaca	1151
Db	1092	aattaaaattccaaagacacagggatctctaacaaatgcaaaaattgaaattcgagacaa	1151
Oy	1152	caatcgttaacgaatcgcgtttcatcgcgtttccaccagttccacaataatcgtlaaactgct	1211
Db	1152	caatcgttaacgaatcgcgtttcatcgcgtttccaccagttccacaataatcgtttaaactgct	1211
Oy	1212	tgcttccaactggtacaaatcgttcagatcgaacgcttcctctgcacctctgggttgctcttg	1271
Db	1212	tgcttccaactggttgaacaaatcgttcagatcgaacgcttcctctgcacctctgggttgctcttg	1271
Oy	1272	ggaaatcgtcgcgttgatgaagcgtttggagtggaagctcgcgtgttaa	1317
Db	1272	ggaaatcgtcgcgttgatgaagcgtttggagtggaagctcgcgtgttaa	1317

RESULT	2
LOCUS	ARI69140
DEFINITION	Ari69140 1330 bp DNA
ACCESSION	ARI69140
VERSION	ARI69140.1 GI:17906909
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1330)
TITLE	Kink,J.A., Thallley,B.S. and Stafford,D.C.
JOURNAL	Vaccine and antitoxin for the treatment of C. difficile disease
FEATURES	Patent: US 6290960-A 22-18-SEP-2001:
source	Location/Qualifiers 1..1330 /organism="unknown"
BASE COUNT	400 a 339 c 246 g 345 t
ORIGIN	

Query Match	98.6%	Score 1304.4	DB 6	Length 1330
Best Local Similarity	99.9%	Pred. No. 0		
Matches 1305	Conservative	0	Mismatches 1	Indels 0
				Gaps 0
0Y	12 gatgtacaccttaactgaatatacaagaacatactcaatctccatccctgaacctgcg	71		
Db	12 GCTCTACACCTTACAGAAATACATCAAGAACATCTCATACCTCCACTGTGAACCTGG	71		
0Y	72 ctagaatcccaatcacctgatcagacctgctctgcgtacagctcccaatacaacatcgcttc	131		
Db	72 CTAGAAATCCAAATCACCTGATGAGCCTGTCTGCTGAGCTTCGAAATCAACATCGCTTC	131		
0Y	132 taagaatcaacttcgatccgatccgcagaagaatacgaatccaagctgttcaatctggaacttc	191		
Db	132 TAAAGTTAACTTGGATCGCATGCACAGAAATACATGATCCAGCTGTTCATATGTGAATCTTC	191		
0Y	192 caaaatcgaaagtatattcctgaagaatgctatcgatatacaacactatgtagcaaaaactcttc	251		
Db	192 CAAATCGAAGTTATCTCTGAAGATGCTATGCTATACAACTCATGTAGCAAAAATCTTTC	251		
0Y	252 caactctctcttgatctgcgtatccgaaataactcaacccaatctctctgaagaatgaata	311		
Db	252 CACTCTCTTCTGGATCCGTAATCCGAAATACTCAACTCTCTCTGTGAACAATGAATA	311		
0Y	312 caccatcatcaactgcatggaaaaaaactctggtctggaagaatctctcgtgaactgcgtga	371		
Db	312 CACCATCATCAATGTCATGGAATAAATCTGTGTGGAAATATCTGTGAATACAGGTGA	371		
0Y	372 aatcatctgagactctcagaagaacccagaagaatacaaaagagtggtgatatacaaatacc	431		
Db	372 AATCATCTGAGACTCTCGAGACACTCAGGAATTCAAACAGCGTGTGTATTCAAATACAC	431		
0Y	432 tcagaatgatacaaatctctgataatcaatcgatcgatctctgataccaaccaaa	491		



Oy 672 agaaatcaaaagaccgtctgaacaacaccagtcacatctctgtatctctgaagaactctgggg 731  
 Db 672 AGAAATCAAAAGACCTGTACGACACACCAATCTGTGTCTGTGAAGAACTCTGGGG 731  
 Oy 732 tgaactacgtacgtacgaacaacccgtactacatctgtatctgaatctgaatccgaacaaca 791  
 Db 732 TGAACTACGTGACGACGACCAACCGTACTGATGTGAATCTGTACGATCGAACAATA 791  
 Oy 792 cgtctgcgtcaacaatgtgtatctccggtctacatctgaatgaagtcgggtgttc 851  
 Db 792 CGTTGACGTCACCAATGTGTGTATCCGGGTACTGTGTAAGAGTCCGGTGTTC 851  
 Oy 852 tctatgaactcaacaatctacatctgaactctctccctgtacgtgtgtatccaatctcatat 911  
 Db 852 TGTATGACTACCAACATCTACTCTGACTCTTCCCTGTACGCTGTGCAAAATTCATCAT 911  
 Oy 912 caagaataatcgtctgtgtgaacaagaacataatctgtcgaacaataatgtatctgtatacat 971  
 Db 912 CAAGAATAATCGCTCTGTGTACAGACCAATATCTGTGCAACAATGATCTGTGTATCAT 971  
 Oy 972 caatgtctgtatgaagaacaagaataaccgtctgtgtacccaatgtctctcagagctgtgt 1031  
 Db 972 CAATGTGTGTATGAACAACAAGAAATACCGTCTGGCTACCAATGCTCTCAGGCTGTGT 1031  
 Oy 1032 agaaagaatctgtctgtctctgtgaatacccggaagctgtgtatctgtctcaagtgatctgt 1091  
 Db 1032 AGAAAGATCTGTCTGTCTGTGAATCCCGACCTGTGTATCTGTCTAGAGTGTGT 1091  
 Oy 1092 aatgaataatcaagaacagacagaggtatcactaacaataatgaataatctgcagagacaa 1151  
 Db 1092 AATGAATAATCAAGAACAGACAGGATATCATACAAATGCAAAATGATCTGCAGACAA 1151  
 Oy 1152 caatgtgaacgaatctgtctgtctgtctgtctgtctgtctgtctgtctgtctgtctgtctgt 1211  
 Db 1152 CAATGTGAACGATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1211  
 Oy 1212 tgcctcgaactgtgtacaaatcgtcagaacagctctctctcgaacatctgtgtgtgtctgt 1271  
 Db 1212 TGGTTCGAACGTGTACAAATCGTCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1271  
 Oy 1272 ggaatcgaacccgt 1317  
 Db 1272 GGAAATCATCCGGT 1317  
 RESULT 4  
 LOCUS XU22962 1338 bp DNA linear SYN 08-NOV-1995  
 DEFINITION Synthetic botulinum neurotoxin serotype A Hc fragment (bota) gene,  
 complete cds.  
 ACCESSION U22962  
 VERSION U22962.1 GI:733428  
 KEYWORDS  
 SOURCE synthetic construct.  
 ORGANISM  
 REFERENCE  
 AUTHORS 1 (bases 1 to 1338)  
 TITLE Clayton, M.A., Clayton, J.M., Brown, D.R. and Middlebrook, J.L.  
 PROTECTIVE VACCINATION WITH A RECOMBINANT FRAGMENT OF CLOSTRIDIUM  
 BOTULINUM NEUROTOXIN SEROTYPE A EXPRESSED FROM A SYNTHETIC GENE IN  
 ESCHERICHIA COLI.  
 JOURNAL Infect. Immun. 63 (7), 2738-2742 (1995)  
 MEDLINE 95310035  
 REFERENCE 2 (bases 1 to 1338)  
 AUTHORS Brown, D.R.  
 TITLE Direct Submission  
 JOURNAL Submitted (17-MAR-1995) Douglas R. Brown, Toxicology, U. S. Army  
 Medical Research Institute of Infectious Diseases, Bldg. 1425, Fort  
 Detrick, Frederick, MD 21702-5011, USA  
 FEATURES  
 source 1..1338  
 /organism="synthetic construct"  
 /db\_xref="taxon:12630"

/lab\_host="Escherichia coli"  
 /note="Based on Clostridium botulinum Type A neurotoxin  
 sequence"  
 gene 9..1325  
 /gene="bota"  
 CDS 9..1325  
 /gene="bota"  
 /codon\_start=1  
 /transl\_table=11  
 /product="botulinum neurotoxin serotype A Hc fragment"  
 /protein\_id="AA80610.1"  
 /db\_xref="GI:733429"  
 /translation="MARLSTFEYIKNIIMSLNLRYSNHLIDLSRVASKINIS  
 KYNFDPIKNOILEPNLESSKIEYLKMLIVNYSNENSTSEFMRIRKYNISLNN  
 EYTLINCMENNSGKVLNGLIETLLODPEKORVVKYKQMINISDYINRPIEYV  
 ITNNRLNRSKYLINGRLIDKRPISNGLNTHASNNIRKIDGSRORHRIKRYNLD  
 KLNKEKIDLDQNSGLKIDPMGDILODPIYMLNLDIPNATVDVNVNVRGTN  
 YLKGPGSVMTNTIYLNSSLYRCKEPIKRYASGNDIVRNNDVYINNVVKREYR  
 LATNLSQAGVERKILSALEIPDVGNLSOVVVMKSKNDQGITNCKNHLDDNGNDIGFI  
 GFHQNNTAKLVASNNYNRROTERRSRFLGSMFEIPIVDGNGMERPL"  
 BASE COUNT 401 a 342 c 249 g 346 t  
 ORIGIN  
 Query Match 98.6%; Score 1304.4; DB 12; Length 1338;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 1305; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 12 gatgtctacatctgaatcaacaagaacataacatctcactcgtgaactgtc 71  
 Db 20 GGTGTACTCTACGATGATACATCAAGACATCATCAATACCTCCATCGTGAACCTCGG 79  
 Oy 72 ctctgaatccaatcaactgaatctgtctgtctgtctgtctgtctgtctgtctgtctgtctgt 131  
 Db 80 CTGGAATTCACATCACCTGATGACCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 139  
 Oy 132 taaagttaactctgaatcgaatcgaacaagaatccagctgtctcaatctggaatctctc 191  
 Db 140 TAAAGTAACTTGCATCCATCGACCAACAATCAATCAATCAATCAATCAATCAATCAATCTTC 199  
 Oy 192 caaaatcgaagttatctcgaagaatgatactgtatgaacatctctgtgaagaactcttc 251  
 Db 200 CAAAATCGAAGTTATCTCTGAAGAAATGCTATGTATCAACTCTGTATGCAAAACTTCTTC 259  
 Oy 252 caccctctctgtgtatcgtatccgaaatcactcaactcactcctctcgaacaatgata 311  
 Db 260 CACCTCTCTGTGATCCGATCCCAAAATACTTCACTCATCTCTGTGACAAATGAATA 319  
 Oy 312 caccatcaactgatacgaagaacaactctgtgtgtgaagaatctctcgtgaactgata 371  
 Db 320 CACCATCATCACTGATGAGAAACAAATCTGTGTGGAAGATATCTGTGAACCTACGCTGA 379  
 Oy 372 aatcaatcgtgaactctgagagacatcagaanaataaacaagctgtgtatctcaaatc 431  
 Db 380 AATCAATCTGGAATCTGACAGACACTCAGGAATCAAAACACGCTGTGTATCAAAATYACTTC 439  
 Oy 432 tcaatgaatcaaatctctgtgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 491  
 Db 440 TCGATGATCAACATCTCTGACTATCATATCGTGTGATTTGTTACCATCAACAA 499  
 Oy 492 tctgtcgaataatcgaataatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 551  
 Db 500 TCGTGTGAATTAATCCAAAATATCATCAACGCGCTGTATGACACCAACCGATCTC 559  
 Oy 552 caatcgtgtgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 611  
 Db 560 CAATCTGTGATTAATCAACGCTGTATTAATCAATATATTAATCAACGAGCTGTGTCTGA 619  
 Oy 612 cactcaccgtcactcgtgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcgaatcga 671  
 Db 620 CACTCACCGCTACATCTGATCAATTAATCTGTGTGCAAAAGAACTCAACGAA 679  
 Oy 672 agaaatcaaaagaccgtctgaacaacaccagtcacatctctgtatctctgaagaactctgggg 731



```

: FILING DATE: 31-OCT-1989
: ATTORNEY/AGENT INFORMATION:
: NAME: INGOLIA, DIANE E.
: REGISTRATION NUMBER: 40,027
: REFERENCE/DOCKET NUMBER: OPHD-01308
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 705-8410
: TELEFAX: (415) 397-8338
: INFORMATION FOR SEQ ID NO: 22:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1330 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1314
: US-08-405-496a-22

```

Query Match Best Local Similarity 98.6% Score 1304.4; DB 2; Length 1330;

Matches 1305; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

Oy 12 gatgtcaacctcactgaatatacaagaacatcaatcaatccatccatcgaactg 71
Db 12 GCTGTCACTCCTCACTGAATATCAAGAAACATCATCATCTCCATCTGAACTGCG 71
Oy 72 ctacgaatccaatccaatcgaactgctgctgctgctgctgctgctgctgctgct 131
Db 72 CTACGAATCCAAATCACTGATGATGATGATGATGATGATGATGATGATGATGATG 131
Oy 132 taagaatcaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactc 191
Db 132 TAAAGTAACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 191
Oy 192 caaatacgaatcgaactcgaactcgaactcgaactcgaactcgaactcgaactcga 251
Db 192 CAAATATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 251
Oy 252 caactcctcctggaactcgaactcgaactcgaactcgaactcgaactcgaactcga 311
Db 252 CACTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 311
Oy 312 caactcctcctggaactcgaactcgaactcgaactcgaactcgaactcgaactcga 371
Db 312 CACTCTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 371
Oy 372 aatcattcgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactc 431
Db 372 AATCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
Oy 432 tcagatgaatcaatcgaactcgaactcgaactcgaactcgaactcgaactcgaactc 491
Db 432 TCAGATGATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 491
Oy 492 tcgtctgaatcaatcgaactcgaactcgaactcgaactcgaactcgaactcgaactc 551
Db 492 TCGTCTGAATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 551
Oy 552 caactcgtggaatcgaactcgaactcgaactcgaactcgaactcgaactcgaactcga 611
Db 552 CAATCTGATGATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 611
Oy 612 cactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactc 671
Db 612 CACTCAGCTGATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 671
Oy 672 agaatcgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactc 731
Db 672 AGAATCAAGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 731

```

```

Oy 732 tgactactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcga 791
Db 732 TGACTACTCGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 791
Oy 792 cgttgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcga 851
Db 792 CGTTGACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 851
Oy 852 tcttgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcga 911
Db 852 TCTTGAATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 911
Oy 912 caagaatcgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcga 971
Db 912 CAGAATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 971
Oy 972 caatgtctgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcga 1031
Db 972 CAATGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1031
Oy 1032 agaaatcgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcga 1091
Db 1032 AGAATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1091
Oy 1092 aatgaatcgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcga 1151
Db 1092 AATGAATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1151
Oy 1152 caatgtcgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcga 1211
Db 1152 CAATGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1211
Oy 1212 tcttgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcga 1271
Db 1212 TCTTGAATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1271
Oy 1272 ggaatcgaactcgaactcgaactcgaactcgaactcgaactcgaactcgaactcga 1317
Db 1272 GGAATCAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1317

```

```

RESULT 3
US-08-915-436-22
: Sequence 22 Application US/08915136
: Patent No. 6290960
: GENERAL INFORMATION:
: APPLICANT: KINK, JOHN A.
: APPLICANT: THALEY, BRUCE S.
: APPLICANT: PADHYE, NISHA V.
: APPLICANT: FIRCA, JOSEPH R.
: APPLICANT: STAFFORD, DOUGLAS C.
: TITLE OF INVENTION: VACCINE AND ANTITOXIN FOR TREATMENT AND
: PREVENTION OF C. DIFFICILE DISEASE
: NUMBER OF SEQUENCES: 32
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MEDLEN & CARROLL, LLP
: STREET: 220 MONTGOMERY STREET, SUITE 2200
: CITY: SAN FRANCISCO
: STATE: CALIFORNIA
: COUNTRY: UNITED STATES OF AMERICA
: ZIP: 94104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/915,136
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/480,604
: FILING DATE:

```